

RAW SEQUENCE LISTING DATE: 05/04/2000
PATENT APPLICATION: US/09/183,972A TIME: 13:19:57

Input Set : A:\Via02701.app
Output Set: C:\CRF3\REFHOLD\05042000\I183972A.raw

3 <110> APPLICANT: Hageman, Gregory S.
4 Kuehn, Markus H.
6 <120> TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
7 ON A NOVEL HUMAN GENE FAMILY
9 <130> FILE REFERENCE: UIA-027.01
11 <140> CURRENT APPLICATION NUMBER: 09/183,972A
12 <141> CURRENT FILING DATE: 1998-10-29
14 <160> NUMBER OF SEQ ID NOS: 49
16 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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862 <210> SEQ ID NO: 6
863 <211> LENGTH: 1241
864 <212> TYPE: PRT
865 <213> ORGANISM: Homo sapiens
867 <400> SEQUENCE: 6
868 Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
869 1 5 10 15
871 Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
872 20 25 30
874 Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu
875 35 40 45
877 Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln
878 50 55 60
880 Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg
881 65 70 75 80
883 Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser
884 85 90 95
886 Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
887 100 105 110
889 Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu
890 115 120 125
892 Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
893 130 135 140
895 Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
896 145 150 155 160
898 His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
899 165 170 175
901 Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
902 180 185 190
904 Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
905 195 200 205
907 Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser
908 210 215 220
910 Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu

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911 225                      230                      235                      240
913 Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
914                      245                      250                      255
916 Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu
917                      260                      265                      270
919 Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys
920                      275                      280                      285
922 Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly
923                      290                      295                      300
925 Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn
926 305                      310                      315                      320
928 Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His
929                      325                      330                      335
931 Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser
932                      340                      345                      350
934 Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu
935                      355                      360                      365
937 Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn
938                      370                      375                      380
940 Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr
941 385                      390                      395                      400
943 Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ile Leu Asp Asn Thr
944                      405                      410                      415
946 Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr Ser Ser Ile
947                      420                      425                      430
949 Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr Gly Arg Glu
950                      435                      440                      445
952 Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr His Lys Leu
953                      450                      455                      460
955 Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu Val Leu Glu
956 465                      470                      475                      480
958 Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val Leu Gln Thr
959                      485                      490                      495
961 Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser His Leu Val
962                      500                      505                      510
964 Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe Leu Ser Ile
965                      515                      520                      525
967 Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro Lys Glu Thr
968                      530                      535                      540
970 Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser Ser Pro Tyr
971 545                      550                      555                      560
973 Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr Ser Lys Val
974                      565                      570                      575
976 Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala Ser Met Glu
977                      580                      585                      590
979 Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser Gly Gln Lys
980                      595                      600                      605
982 Val Asp Leu Ile Thr Trp Pro Trp Ser Glu Thr Ser Ser Glu Lys Ser
983                      610                      615                      620

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985 Ala Glu Pro Leu Ser Lys Pro Trp Leu Glu Asp Asp Asp Ser Leu Leu
986 625 630 635 640
988 Pro Ala Glu Ile Glu Asp Lys Lys Leu Val Leu Val Asp Lys Met Asp
989 645 650 655
991 Ser Thr Asp Gln Ile Ser Lys His Ser Lys Tyr Glu His Asp Asp Arg
992 660 665 670
994 Ser Thr His Phe Pro Glu Glu Glu Pro Leu Ser Gly Pro Ala Val Pro
995 675 680 685
997 Ile Phe Ala Asp Thr Ala Ala Glu Ser Ala Ser Leu Thr Leu Pro Lys
998 690 695 700
1000 His Ile Ser Glu Val Pro Gly Val Asp Asp Cys Ser Val Thr Lys Ala
1001 705 710 715 720
1003 Pro Leu Ile Leu Thr Ser Val Ala Ile Ser Ala Ser Thr Asp Lys Ser
1004 725 730 735
1006 Asp Gln Ala Asp Ala Ile Leu Arg Glu Asp Met Glu Gln Ile Thr Glu
1007 740 745 750
1009 Ser Ser Asn Tyr Glu Trp Phe Asp Ser Glu Val Ser Met Val Lys Pro
1010 755 760 765
1012 Asp Met Gln Thr Leu Trp Thr Ile Leu Pro Glu Ser Glu Arg Val Trp
1013 770 775 780
1015 Thr Arg Thr Ser Ser Leu Glu Lys Leu Ser Arg Asp Ile Leu Ala Ser
1016 785 790 795 800
1018 Thr Pro Gln Ser Ala Asp Arg Leu Trp Leu Ser Val Thr Gln Ser Thr
1019 805 810 815
1021 Lys Leu Pro Pro Thr Thr Ile Ser Thr Leu Leu Glu Asp Glu Val Ile
1022 820 825 830
1024 Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile Gly Thr Asp
1025 835 840 845
1027 Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys Val Gly Ser
1028 850 855 860
1030 Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met Val Ser Val
1031 865 870 875 880
1033 Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr Gln Thr Ser
1034 885 890 895
1036 Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn Met Met Phe
1037 900 905 910
1039 Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys Ala Leu Glu
1040 915 920 925
1042 Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser Asn Leu Thr
1043 930 935 940
1045 Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Ile Val
1046 945 950 955 960
1048 Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro Asn Val Asn
1049 965 970 975
1051 Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr Ala Tyr Asn
1052 980 985 990
1054 Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val Glu Ser Gly
1055 995 1000 1005
1057 Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu Phe Ser Glu

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1058      1010      1015      1020
1060 Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg Cys Phe Pro
E--> 1061/025      1030      1035      1040
1063 Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu Cys Asp Leu
1064      1045      1050      1055
1066 Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile Met Pro Gly
1067      1060      1065      1070
1069 His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp Trp Tyr Arg
1070      1075      1080      1085
1072 Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile Ile Gly Ile
1073      1090      1095      1100
1075 Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser Ala Ile Ile
E--> 1076/105      1110      1115      1120
1078 Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg Ser Glu Arg
1079      1125      1130      1135
1081 Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser Leu Ser Ser
1082      1140      1145      1150
1084 Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser His Arg Ala
1085      1155      1160      1165
1087 Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro Phe Tyr Ser
1088      1170      1175      1180
1090 Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg
E--> 1091/185      1190      1195      1200
1093 Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg
1094      1205      1210      1215
1096 Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe Ala Ala Phe
1097      1220      1225      1230
1099 Val Arg Glu Gln Gln Val Glu Glu Val
1100      1235      1240

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VERIFICATION SUMMARY

DATE: 05/04/2000

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TIME: 13:19:58

Input Set : A:\Via02701.app

Output Set: C:\CRF3\REFHOLD\05042000\I183972A.raw

L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1061 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:1132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

STATISTICS SUMMARY DATE: 05/04/2000
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Application Serial Number: US/09/183,972
Alpha or Numeric: Numeric
Application Class: 536
Application File Date: 10-29-1998
Art Unit: 1644
Software Application: PatentIn
Total Number of Sequences: 49
Number of Errors: 3
Number of Warnings: 10
Number of Corrections: 0

MESSAGE SUMMARY

332 E: 3 ((32) Invalid/Missing Amino Acid Numbering)
341 W: 10 ((46) "n" or "Xaa" used)